Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Currently amended) A method for determining the likelihood that a human subject has major depression disorder, the method comprising the steps of:

(i) isolating a subject's brain tissue, wherein the brain tissue is dorsolateral prefrontal cortex tissue;

(ii) contacting the subject's isolated brain tissue with a nucleic acid probe which is at least 95% complementary to SEQ ID NO:1 ~~mRNA encoding FGFR2~~;

(iii) detecting the level of probe that ~~selectively~~ associates with said subject's FGFR2 mRNA ~~said polynucleotide~~; and

(iv) comparing the detected level of ~~selectively~~ associated probe with a control, whereby if the detected level is less than the control, an increased likelihood that the subject has major depression disorder is determined; and whereby, if the detected level is not less than the control, an increase in said likelihood is not determined by the method.

2.-30. (Canceled)

31. (Currently amended) The method of claim 1, wherein said nucleic acid probe is fully complementary to SEQ ID NO:1 ~~mRNA encoding FGFR2~~.

32. (Currently amended) A method for determining the likelihood that a deceased human subject had major depression disorder, the method comprising the steps of:

(i) isolating a subject's brain tissue, wherein the brain tissue is dorsolateral prefrontal cortex tissue;

(ii) contacting the subject's isolated brain tissue with a nucleic acid probe which is at least 95% complementary to SEQ ID NO:1 ~~mRNA encoding FGFR2~~;

(iii) detecting the level of probe that ~~selectively~~ associates with said subject's FGFR2 mRNA ~~said polynucleotide~~; and

(iv) comparing the detected level of ~~selectively~~ associated probe with a control, whereby if the detected level is less than the control, an increased likelihood that the subject has major depression disorder is determined; and whereby, if the detected level is not less than the control, an increase in said likelihood is not determined by the method.

33. (Currently amended) The method of claim 32, wherein said nucleic acid probe is fully complementary to SEQ ID NO:1 ~~mRNA encoding FGFR2~~.

34. (New) The method of claim 1, wherein said probe is at least 95% identical to the full-length complement of SEQ ID NO:1.

35. (New) The method of claim 32, wherein said probe is at least 95% identical to the full-length complement of SEQ ID NO:1.